REMARKS

This application has been carefully reviewed in light of the Office Action dated December 21, 2005. Claims 2 to 6, 10 and 11 are in the application, with Claims 2 and 10 being independent. Claims 1 and 9 have been cancelled without prejudice. Claims 10 and 11 have been newly added. Reconsideration and further examination are respectfully requested.

Claims 1 to 6 and 9 have been rejected under 35 U.S.C. § 102(e) over U.S. Patent No. 6,228,575 (Gingeras). (It is Applicants' understanding that Gingeras is inadvertently referred to as "Chee" at pages 5 and 6 of the Office Action.) The rejections are respectfully traversed.

Claim 2 recites, *inter alia*, the following steps: (c) analyzing the first template pattern to locate probes and to calculate a mean value of fluorescence intensities (Fi) of the double-stranded nucleic acids having i of mismatched base pairs, where i is an integer not less than 1; (d) calculating a difference (F1, 0) between the fluorescence intensity of the fully complementary double-stranded nucleic acid without mismatch (F0) and the mean value of the fluorescence intensities of the double-stranded nucleic acids having one-base mismatch (F1), further calculating a difference (Fi+1, i) between a fluorescence intensity of a double-stranded nucleic acid having (i+1) base mismatches (Fi+1) and a fluorescence intensity of a double-stranded nucleic acid having i-base mismatches (Fi), and identifying i being Fi+1, i << Fi, i-1; and (e) preparing a second template pattern of positive probe spots of probes having base sequences differing from the base sequence of the second probe by i or less bases where i is determined in said step (d), wherein negative probe spots are probes having base sequences differing from the second

probe by more than i bases. Claim 10 recites, *inter alia*, a threshold value is set up between a fluorescence intensity corresponding to i base mismatch(es) and a fluorescence intensity corresponding to i+1 base mismatches, where i is an integer not less than 1, such that a probe location showing a fluorescence intensity above the threshold value is defined to be positive while a probe location otherwise is defined to be negative, and the template pattern and the sample pattern are prepared by adopting only positive probe locations. By virtue of these features, it is possible to reduce the influence of unstable multiple base mismatches on measurement, and thereby achieve an analysis with higher precision and efficiency.

Gingeras is not seen to teach or suggest at least the above-discussed features.

As Applicants understand it, Gingeras merely discloses comparing a hybridization pattern of a target nucleic acid derived from a living organism with hybridization patterns stored in a database, to identify the genus or species of the living organism.

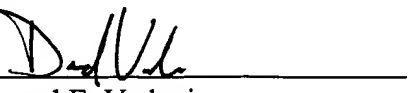
In this regard, as set forth at MPEP 2131, a claim is anticipated only if the identical invention is shown as in as complete detail as is contained in the claim.

The dependent claims are also submitted to be patentable because they set forth additional aspects of the present invention and are dependent from the independent claims discussed above. Therefore, separate and individual consideration of each dependent claim is respectfully requested.

The application is believed to be in condition for allowance, and a Notice of Allowance is respectfully requested.

Applicants' undersigned attorney may be reached in our Costa Mesa, California office by telephone at (714) 540-8700. All correspondence should be directed to our address given below.

Respectfully submitted,



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